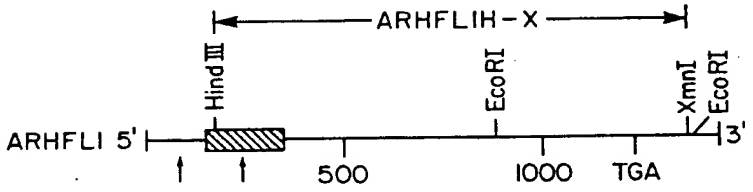
FIGURE 1

A.

Oligo A Complement	5'-ACC	TGT	GAG	GGC	TGT	AAG	GTC	TTC	TTC	AAA	AG-3'	(100%)
	**	***	*	*	**	***	***	***	***	***	**	
hAR (X)	ACA	TGT	GGA	AGC	TGC	AAG	GTC	TTC	TTC	AAA	AG	(84%)
hPR (11)	ACC	TGT	GGG	AGC	TGT	AAG	GTC	TTC	TTT	AAG	AG	(88%)
hMR (4)	ACC	TGT	GGC	AGC	TGC	AAA	GTT	TTC	TTC	AAA	AG	(81%)
hGR (5)	ACT	TGT	GGA	AGC	TGT	AAA	GTT	TTC	TTC	AAA	AG	(81%)
hER (6)	TCC	TGT	GAG	GGC	TGT	AAG	GCC	TTC	TTC	AAG	AG	(91%)
hT3R (3, 17)	ACG	TGT	GAA	GGC	TGC	AAG	GGT	TTC	TTT	AGA	AG	(78%)
hRAR (17)	GCC	TGT	GAG	GGC	TGC	AAG	GGC	TTC	TTC	CGC	CG	(78%)

B.



C.

DNA-Binding Domain

		+	+		10			+	20+					30		
hAR		C	L	I	C	G	D	E	A	S	G	C	H	Y	G	A	L	T	C	G	S	C	K	V	F	F	K	R	A	A	E	G	(100%)
hPR	(aa 567)	C	L	I	C	G	D	E	A	S	G	C	H	Y	G	V	L	T	C	G	S	C	K	V	F	F	K	R	A	M	E	G	(94%)
hMR	(aa 603)	C	L	V	C	G	D	E	A	S	G	C	H	Y	G	V	V	T	C	G	S	C	K	V	F	F	K	R	A	V	E	G	(87%)
hGR	(aa 421)	C	L	V	C	S	D	E	A	S	G	C	H	Y	G	V	L	T	C	G	S	C	K	V	F	F	K	R	A	V	E	G	(87%)
hER	(aa 185)	C	A	V	C	N	D	Y	A	S	G	Y	H	Y	G	V	W	S	C	E	G	C	K	A	F	F	K	R	S	I	Q	G	(55%)
cVDR		C	G	V	C	G	D	R	A	T	G	F	H	F	N	A	M	T	C	E	G	C	K	G	F	F	R	R	S	M	K	R	(48%)
hT3R	(aa 102)	C	V	V	C	G	D	K	A	T	G	Y	H	Y	R	C	I	T	C	E	G	C	K	G	F	F	R	R	T	I	Q	K	(48%)
vERBA	(aa 37)	C	V	V	C	G	D	K	A	T	G	Y	H	Y	R	C	I	T	C	E	G	C	K	S	F	F	R	R	T	I	Q	K	(48%)
hRAR	(aa 58)	C	F	V	C	Q	D	K	S	S	G	Y	H	Y	G	V	S	A	C	E	G	C	K	G	F	F	R	R	S	I	Q	K	(45%)

					+		40		+				50		+		+		60+					
hAR			K	Q	K	Y	L	C	A	S	R	N	D	C	T	I	D	K	F	R	R	K	N	C	P	S	C	R	L	R	K	C	Y	E	A	G	M	(100%)
hPR			Q	H	N	Y	L	C	A	G	R	N	D	C	I	V	D	K	I	R	R	K	N	C	P	A	C	R	L	R	K	C	C	Q	A	G	M	(71%)
hMR			Q	H	N	Y	L	C	A	G	R	N	D	C	I	I	D	K	I	R	R	K	N	C	P	A	C	R	L	Q	K	C	L	Q	A	G	M	(71%)
hGR			Q	H	N	Y	L	C	A	G	R	N	D	C	I	I	D	K	I	R	R	K	N	C	P	A	C	R	Y	R	K	C	L	Q	A	G	M	(71%)
hER			H	N	D	Y	M	C	P	A	T	N	Q	C	T	I	D	K	N	R	R	K	S	C	Q	A	C	R	L	R	K	C	Y	E	V	G	M	(63%)
cVDR			K	A	M	F	T	C	P	F	N	G	D	C	K	I	T	K	D	N	R	R	H	C	Q	A	C	R	L	K	R	C	V	D	I	G	M	(40%)
hT3R		N	L	H	P	S	Y	S	C	K	Y	E	G	K	C	V	I	D	K	V	T	R	N	Q	C	Q	E	C	R	F	K	K	C	I	Y	V	G	M	(40%)
vERBA		N	L	H	P	T	T	S	C	T	Y	D	G	C	C	V	I	D	K	I	T	R	N	Q	C	Q	L	C	R	F	K	K	C	I	S	V	G	M	(37%)
hRAR			N	M	V	Y	T	C	H	R	D	K	N	C	I	I	N	K	V	T	R	N	R	C	Q	Y	C	R	L	Q	K	C	F	E	V	G	M	(43%)

FIGURE 2

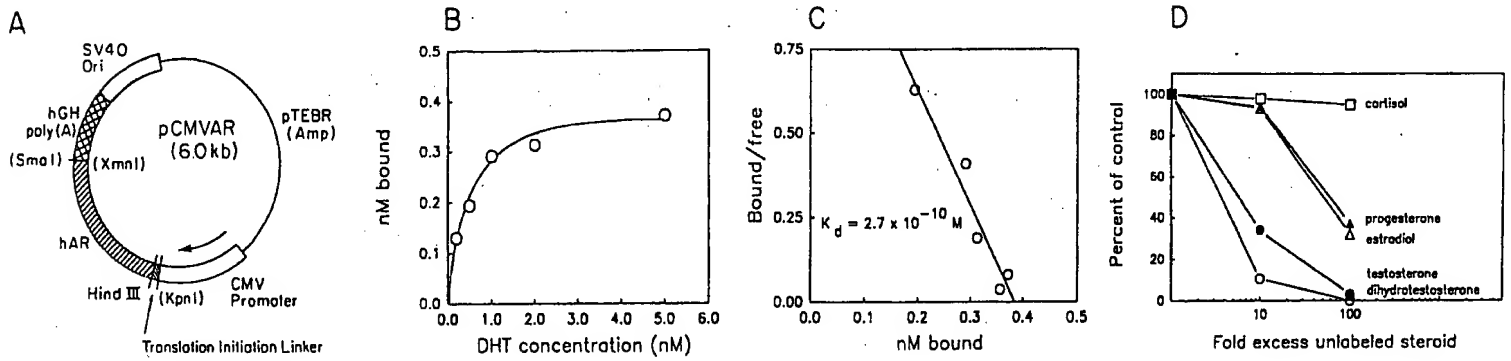

A
SV40 Ori
hGH poly(A)
(SmaI)
(XmnI)
pCMVAR (6.0kb)
pTEBR (Amp)
hAR
Hind III
(KpnI)
CMV Promoter
Translation Initiation Linker
B
nM bound
DHT concentration (nM)
C
Bound/free
$K_d = 2.7 \times 10^{-10}$ M
nM bound
D
Percent of control
cortisol
progesterone
estradiol
testosterone
dihydrotestosterone
Fold excess unlabeled steroid

FIGURE 3

Compiled Clone Map of the Human Androgen Receptor

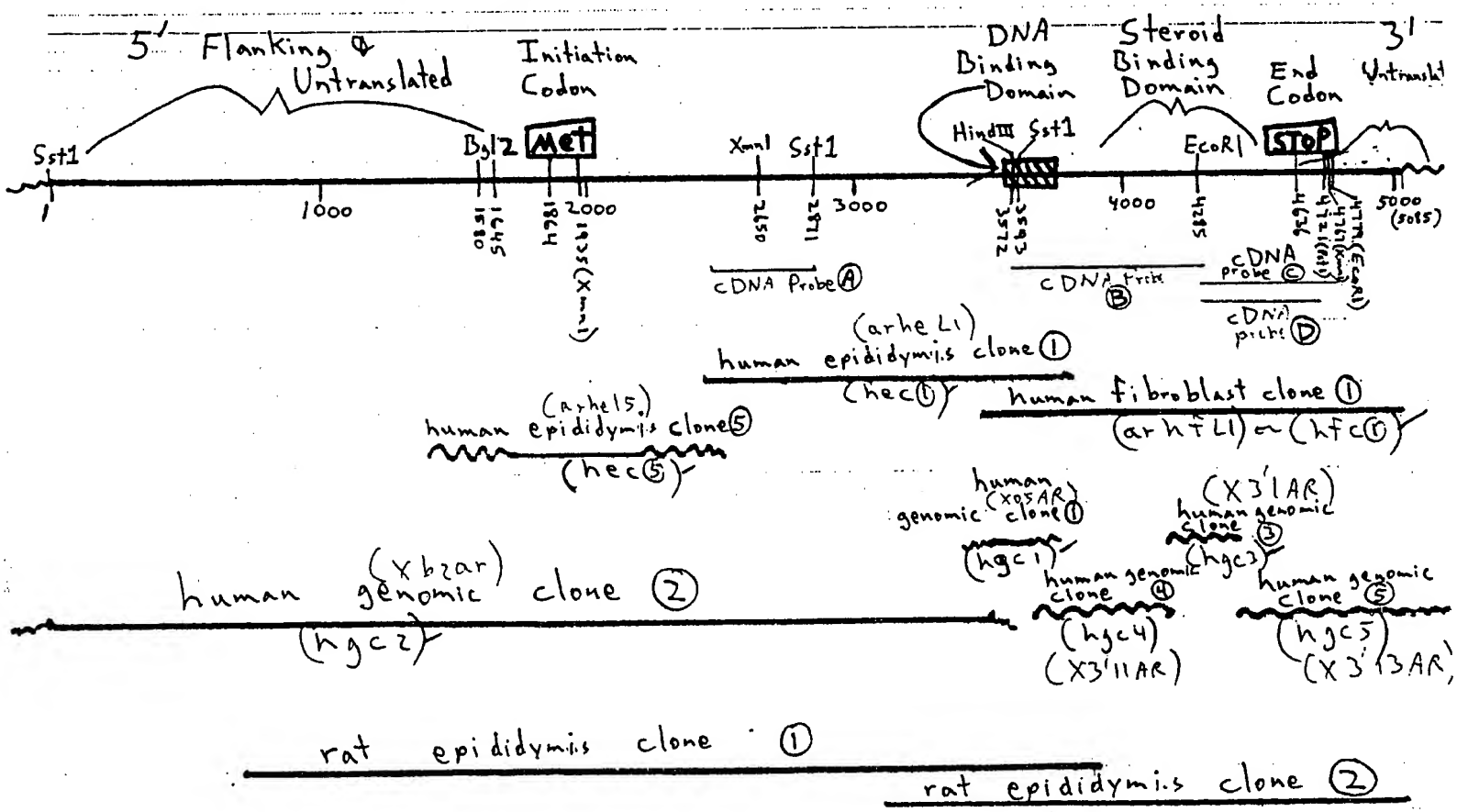


FIGURE 4 (page 1 of 6)

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        10          20          30          40          50          60
GAGCTCTGGA CAAAATTGAG CGCCTATGTG TACATGGCAA GTGTTTTTAG TGTTTGTGTG
CTCGAGACCT GTTTTAACTC GCGGATACAC ATGTACCGTT CACAAAAATC ACAAACACAC

        70          80          90          100         110         120
TTTACCTGCT TGTCTGGGTG ATTTTGCCTT TGAGAGTCTG GATGAGAAAT GCATGGTTAA
AAATGGACGA ACAGACCCAC TAAAACGGAA ACTCTCAGAC CTACTCTTTA CGTACCAATT

        130         140         150         160         170         180
AGGCAATTCC AGACAGGAAG AAAGGCAGAG AAGAGGGTAG AAATGACCTC TGATTCTTGG
TCCGTTAAGG TCTGTCCTTC TTTCCGTCTC TTCTCCCATC TTTACTGGAG ACTAAGAACC

        190         200         210         220         230         240
GGCTGAGGGT TCCTAGAGCA AATGGCACAA TGCCACGAGG CCCGATCTAT CCCTATGACG
CCGACTCCCA AGGATCTCGT TTACCGTGTT ACGGTGCTCC GGGCTAGATA GGGATACTGC

        250         260         270         280         290         300
GAACTCTAAG GTTTCAGCAT CAGCTATCTG CTGGCTTGGT CACTGGCTTG CCTCCTCAGT
CTTGAGATTC CAAAGTCGTA GTCGATAGAC GACCGAACCA GTGACCGAAC GGAGGAGTCA

        310         320         330         340         350         360
TTGTAGGAGA CTCTCCCACT CTCCCATCTG CGCGCTCTTA TCAGTCCTGA AAAGAACCCN
AACATCCTCT GAGAGGGTGA GAGGGTAGAC GCGCGAGAAT AGTCAGGACT TTTCTTGGGN

        370         380         390         400         410         420
TGGCNAGCCA GGAGCNAGGT ATTCNTATCG TCCTTTTCNT CCTCCTNGCC TCACCTNGTT
ACCGNTCGGT CCTCGNTCCA TAAGNATAGC AGGAAAAGNA GGAGGANCGG AGTGGANCAA

        430         440         450         460         470         480
GNTTTTTAGA TTGGNCTTNG NAACCAAATT TGTATGCTGG CCTCCAGGAA ATCTGGAGCC
CNAAAAATCT AACCNGAANC NTTGGTTTAA ACATACGACC GGAGGTCCTT TAGACCTCGG

        490         500         510         520         530         540
TGGCGCCTAA ACCTTGGTTT AGGAAAGCAG GAGCTATTCA GGAAGCAGGG TCCTCCAGGG
ACCGCGGATT TGGAACCAAA TCCTTTCGTC CTCGATAAGT CCTTCGTCCC AGGAGGTCCC

        550         560         570         580         590         600
CTAGAGCTAG CCTCTCCTGC CCTCGCCCAC GTGCGCCAGC ACTTGTTTCT CCAAAGCNAC
GATCTCGATC GGAGAGGACG GGAGCGGGTG CACGCGGTCG TGAACAAAGA GGTTTCGNTG

        610         620         630         640         650         660
TAGGCAGGCG TTAGCGCGCG GTGAGGGGAG GGGAGAAAAG GAAAGGGGAG GGGAGGGAAA
ATCCGTCCGC AATCGCGCGC CACTCCCCTC CCCTCTTTTC CTTTCCCCTC CCCTCCCTTT

        670         680         690         700         710         720
AGGAGGTGGG AAGGCAAGGA GGCCGGCCNG GTGGGGGCGG GACCCGACTC GCANNAACTG
TCCTCCACCC TTCCGTTCCT CCGGCCGGNC CACCCCCGCC CTGGGCTGAG CGTNNTTGAC

        730         740         750         760         770         780
TTGCATTTGC TCTCCACCTC CCAGCGCCCC CTCCGAGATC CCGGGGAGCC AGCTTGCTGG
AACGTAAACG AGAGGTGGAG GGTCGCGGGG GAGGCTCTAG GGCCCCTCGG TCGAACGACC

        790         800         810         820         830         840
GAGAGCGGGA ACGGTCCGGA GCAAGCCCAG AGGCAGAGGA GGCGACAGAG GGAAAAAGGG
CTCTCGCCCT TGCCAGGCCT CGTTCGGGTC TCCGTCTCCT CCGCTGTCTC CCTTTTTCCC

        850         860         870         880         890         900
CCCNAGCTAG CCGCTCCAGT GCTGTACAGN AGCCGAAGGA CGCACCACGC CAGCCCCAGC
GGGNTCGATC GGCGAGGTCA CGACATGTCN TCGGCTTCCT GCGTGGTGCG GTCGGGGTCG
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FIGURE 4 (page 2 of 6)

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       910        920        930        940        950        960
CCGGCTCCAG CGACAGCNAA CGCCTCTTGC ANGCGTTCGA AGCCGCCGCC CGGAGCTGCC
GGCCGAGGTC GCTGTCGNTT GCGGAGAACG TNCGCAAGCT TCGGCGGCGG GCCTCGACGG

       970        980        990       1000       1010       1020
CTTTCCTCTT CGGTGAAGTT TTTAAAAGCT GCTAAAGACT CGGAGGAAGC AAGGAAAGTG
GAAAGGAGAA GCCACTTCAA AAATTTTCGA CGATTTCTGA GCCTCCTTCG TTCCTTTCAC

      1030       1040       1050       1060       1070       1080
CCTGGTAGGA CTGACGGCTG CCTTTGTCCT CCTCCTCTCC ACCCCGCCTC CCCCCACCCT
GGACCATCCT GACTGCCGAC GGAAACAGGA GGAGGAGAGG TGGGGCGGAG GGGGGTGGGA

      1090       1100       1110       1120       1130       1140
GCCTTCCCCC CCTCCCCCGT CTTCTCTCCC GCAGCTGCCT CAGTCGGCTA CTCTCAGCCA
CGGAAGGGGG GGAGGGGGCA GAAGAGAGGG CGTCGACGGA GTCAGCCGAT GAGAGTCGGT

      1150       1160       1170       1180       1190       1200
ACCCCCCTCA CCACCCTTCT CCCCACCCGC CCCCCCGCCC CCGTCGGCCC AGCGNTGNCA
TGGGGGGAGT GGTGGGAAGA GGGGTGGGCG GGGGGGCGGG GGCAGCCGGG TCGCNACNGT

      1210       1220       1230       1240       1250       1260
GNCCGAGTTT GCAGAGAGGT AACTCCCTTT GGCTGCGAGC GGGCGAGNCT AGCTGCACAT
CNGGCTCAAA CGTCTCTCCA TTGAGGGAAA CCGACGCTCG CCCGCTCNGA TCGACGTGTA

      1270       1280       1290       1300       1310       1320
TGCAAAGAAG GCTCTTAGGA GCAGGCGACT GGGGAGCGGC TTCAGCACTG CAGCCACGAC
ACGTTTCTTC CGAGAATCCT CGTCCGCTGA CCCCTCGCCG AAGTCGTGAC GTCGGTGCTG

      1330       1340       1350       1360       1370       1380
CNGCCTGSTT AGGCTGCACG CGGAGAGAAC CCTCTGTTTT CCCCCACTCT CTCTCCACCT
GNCGGACCAA TCCGACGTGC GCCTCTCTTG GGAGACAAAA GGGGGTGAGA GAGAGGTGGA

      1390       1400       1410       1420       1430       1440
CCTCCTGCCT TCCCCACCCC GAGTGCGGAG CCAGAGATCA AAAGATGAAA AGGCAGTCAG
GSAGGACGGA AGGGGTGGGG CTCACGCCTC GGTCTCTAGT TTTCTACTTT TCCGTCAGTC

      1450       1460       1470       1480       1490       1500
GTCTTCAGTA GCCAAAAAAC AAAACAAACA AAAACAAAAA AGCCGAAATA AAAGAAAAAG
CAGAAGTCAT CGGTTTTTTG TTTTGTTTGT TTTTGTTTTT TCGGCTTTAT TTTCTTTTTC

      1510       1520       1530       1540       1550       1560
ATAATAACTC AGTTCTTATT TGCACCTACT TCAGTGGACA CTGAATTTGG AAGGTGGAGG
TATTATTGAG TCAAGAATAA ACGTGGATGA AGTCACCTGT GACTTAAACC TTCCACCTCC

      1570       1580       1590       1600       1610       1620
ATTTTGTTTT TTTCTTTTAA GATCTGGGCA TCTTTTGAAT CTACCCTTCA AGTATTAAGA
TAAAACAAAA AAAGAAAATT CTAGACCCGT AGAAAACTTA GATGGGAAGT TCATAATTCT

      1630       1640       1650       1660       1670       1680
GACAGACTGT GAGCCTAGCA GGGCAGATCT TGTCCACCGT GTGTCTTCTT CTGCACGAGA
CTGTCTGACA CTCGGATCGT CCCGTCTAGA ACAGGTGGCA CACAGAAGAA GACGTGCTCT

      1690       1700       1710       1720       1730       1740
CTTTGAGGCT GTCAGAGCGC TTTTTGCGTG GTTGCTCCCG CAAGTTTCCT TCTCTGGAGC
GAAACTCCGA CAGTCTCGCG AAAAACGCAC CAACGAGGGC GTTCAAAGGA AGAGACCTCG

      1750       1760       1770       1780       1790       1800
TTCCCGCAGG TGGGCAGCTA GCTGCAGCGA CTACCGCATC ATCACAGCCT GTTGAACTCT
AAGGGCGTCC ACCCGTCGAT CGACGTCGCT GATGGCGTAG TAGTGTCGGA CAACTTGAGA
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FIGURE 4 (page 3 of 6)

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      1810       1820       1830       1840       1850       1860
TCTGAGCAAG AGAAGGGGAG GCGGGGTAAG GGAAGTAGGT GGAAGATTCA GCCAAGCTCA
AGACTCGTTC TCTTCCCCTC CGCCCCATTC CCTTCATCCA CCTTCTAAGT CGGTTCGAGT

      1870       1880       1890       1900       1910       1920
AGGATGGAAG TGCAGTTAGG GCTGGGAAGG GTCTACCCTC GGCCGCCGTC CAAGACCTAC
TCCTACCTTC ACGTCAATCC CGACCCTTCC CAGATGGGAG CCGGCGGCAG GTTCTGGATG

      1930       1940       1950       1960       1970       1980
CGAGGAGCTT TCCAGAATCT GTTCCAGAGC GTGCGCGAAG TGATCCAGAA CCCGGGCCCC
GCTCCTCGAA AGGTCTTAGA CAAGGTCTCG CACGCGCTTC ACTAGGTCTT GGGCCCGGGG

      1990       2000       2010       2020       2030       2040
AGGCACCCAG AGGCCGCGAG CGCAGCACCT CCCGGCGCCA GTTTGCTGCT GCTGCAGCAG
TCCGTGGGTC TCCGGCGCTC GCGTCGTGGA GGGCCGCGGT CAAACGACGA CGACGTCGTC

      2050       2060       2070       2080       2090       2100
CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG
GTCGTCGTCG TCGTCGTCGT CGTCGTCGTC GTCGTCGTCG TCGTCGTCGT CGTCGTCGTC

      2110       2120       2130       2140       2150       2160
CAGCAGCAAG AGACTAGCCC CAGGCAGCAG CAGCAGCAGC AGGGTGAGGA TGGTTCTCCC
GTCGTCGTTC TCTGATCGGG GTCCGTCGTC GTCGTCGTCG TCCCACTCCT ACCAAGAGGG

      2170       2180       2190       2200       2210       2220
CAAGCCCATC GTAGAGGCCC CACAGGCTAC CTGGTCCTGG ATGAGGAACA GCAACCTTCA
GTTCGGGTAG CATCTCCGGG GTGTCCGATG GACCAGGACC TACTCCTTGT CGTTGGAAGT

      2230       2240       2250       2260       2270       2280
CAGCCGCAGT CGGCCCTGGA GTGCCACCCC GAGAGAGGTT GCGTCCCAGA GCCTGGAGCC
GTCGGCGTCA GCCGGGACCT CACGGTGGGG CTCTCTCCAA CGCAGGGTCT CGGACCTCGG

      2290       2300       2310       2320       2330       2340
GCCGTGGCCG CCAGCAAGGG GCTGCCGCAG CAGCTGCCAG CACCTCCGGA CGAGGATGAC
CGGCACCGGC GGTCGTTCCC CGACGGCGTC GTCGACGGTC GTGGAGGCCT GCTCCTACTG

      2350       2360       2370       2380       2390       2400
TCAGCTGCCC CATCCACGTT GTCCCTGCTG GGCCCCACTT TCCCCGGCTT AAGCAGCTGC
AGTCGACGGG GTAGGTGCAA CAGGGACGAC CCGGGGTGAA AGGGGCCGAA TTCGTCGACG

      2410       2420       2430       2440       2450       2460
TCCGCTGACC TTAAAGACAT CCTGAGCGAG GCCAGCACCA TGCAACTCCT TCAGCAACAG
AGGCGACTGG AATTTCTGTA GGACTCGCTC CGGTCGTGGT ACGTTGAGGA AGTCGTTGTC

      2470       2480       2490       2500       2510       2520
CAGCAGGAAG CAGTATCCGA AGGCAGCAGC AGCGGGAGAG CGAGGGAGGC CTCGGGGGCT
GTCGTCCTTC GTCATAGGCT TCCGTCGTCG TCGCCCTCTC GCTCCCTCCG GAGCCCCCGA

      2530       2540       2550       2560       2570       2580
CCCACTTCCT CCAAGGACAA TTACTTAGGG GGCACTTCGA CCATTTCTGA CAACGCCAAG
GGGTGAAGGA GGTTCCTGTT AATGAATCCC CCGTGAAGCT GGTAAAGACT GTTGCGGTTC

      2590       2600       2610       2620       2630       2640
GAGTTGTGTA AGGCAGTGTC GGTGTCCATG GGCCTGGGTG TGGAGGCGTT GGAGCATCTG
CTCAACACAT TCCGTCACAG CCACAGGTAC CCGGACCCAC ACCTCCGCAA CCTCGTAGAC

      2650       2660       2670       2680       2690       2700
AGTCCAGGGG AACAGCTTCG GGGGGATTGC ATGTACGCCC CACTTTTGGG AGTTCCACCC
TCAGGTCCCC TTGTCGAAGC CCCCCTAACG TACATGCGGG GTGAAAACCC TCAAGGTGGG
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FIGURE 4 (page 4 of 6)

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      2710        2720        2730        2740        2750        2760
GCTGTGGCTC CCACTCCTTG TGCCCCATTG GCCGAATGCA AAGGTTCTCT GCTAGACGAC
CGACACCGAG GGTGAGGAAC ACGGGGTAAC CGGCTTACGT TTCCAAGAGA CGATCTGCTG

      2770        2780        2790        2800        2810        2820
AGCCCAGGCA AGAGCACTGA AGATACTGCT GAGTATTCCC CTTTCAAGGG AGGTTACACC
TCGCGTCCGT TCTCGTGACT TCTATGACGA CTCATAAGGG GAAAGTTCCC TCCAATGTGG

      2830        2840        2850        2860        2870        2880
AAAGGGCTAG AAGGCGAGAG CCTAGGCTGC TCTGGCAGCG CTGCAGCAGG GAGCTCCGGG
TTTCCCGATC TTCCGCTCTC GGATCCGACG AGACCGTCGC GACGTCGTCC CTCGAGGCCC

      2890        2900        2910        2920        2930        2940
ACACTTGAAC TGCCGTCTAC CCTGTCTCTC TACAAGTCCG GAGCACTGGA CGAGGCAGCT
TGTGAACTTG ACGGCAGATG GGACAGAGAG ATGTTCAGGC CTCGTGACCT GCTCCGTCGA

      2950        2960        2970        2980        2990        3000
GCGTACCAGA GTCGCGACTA CTACAACTTT CCACTGGCTC TGGCCGGACC GCCGCCCCCT
CGCATGGTCT CAGCGCTGAT GATGTTGAAA GGTGACCGAG ACCGGCCTGG CGGCGGGGGA

      3010        3020        3030        3040        3050        3060
CCGCCGCCTC CCCATCCCCA CGCTCGCATC AAGCTGGAGA ACCCGCTGGA CTACGGCAGC
GGCGGCGGAG GGGTAGGGGT GCGAGCGTAG TTCGACCTCT TGGGCGACCT GATGCCGTCG

      3070        3080        3090        3100        3110        3120
GCCTGGGCGG CTCGGCGGGC GCACTGCCGC TATGGGGACC TGGCGAGCCT GCATGGCGCG
CGGACCCGCC GAGCCGCCCG CGTGACGGCG ATACCCCTGG ACCGCTCGGA CGTACCGCGC
                 CG

      3130        3140        3150        3160        3170        3180
GGTGCAGCGG GACCCGGTTC TGGGTCACCC TCAGCCGCCG CTTCCTCATC CTGGCACACT
CCACGTCGCC CTGGGCCAAG ACCCAGTGGG AGTCGGCGGC GAAGGAGTAG GACCGTGTGA

      3190        3200        3210        3220        3230        3240
CTCTTCACAG CCGAAGAAGG CCAGTTGTAT GGACCGTGTG GTGGTGGTGG GGGTGGTGGC
GAGAAGTGTC GGCTTCTTCC GGTCAACATA CCTGGCACAC CACCACCACC CCCACCACCG

      3250        3260        3270        3280        3290        3300
GGCGGCGGCG GCGGCGGCGG CGGCGGCGGC GGCGGCGGCG CGAGGCGGGA
CCGCCGCCGC CGCCGCCGCC GCCGCCGCCG CCGCCGCCGC GCTCCGCCCT

      3310        3320        3330        3340        3350        3360
GCTGTAGCCC CCTACGGCTA CACTCGGCCC CCTCAGGGGC TGGCGGCCA GGAAAGCGAC
CGACATCGGG GGATGCCGAT GTGAGCCGGG GGAGTCCCCG ACCGCCCGGT CCTTTCGCTG

      3370        3380        3390        3400        3410        3420
TTCACCGCAC CTGATGTGTG GTACCCTGGC GGCATGGTGA GCAGAGTGCC CTATCCCAGT
AAGTGGCGTG GACTACACAC CATGGGACCG CCGTACCACT CGTCTCACGG GATAGGGTCA

      3430        3440        3450        3460        3470        3480
CCCACTTGTG TCAAAAGCGA AATGGGCCCC TGGATGGATA GCTACTCCCG GGAACCTTAC
GGGTGAACAC AGTTTTCGCT TTACCCGGGG ACCTACCTAT CGATGAGGGC CCTTGGAATG

      3490        3500        3510        3520        3530        3540
GGGGACATGC GTTTGGAGAC TGCCAGGGAC CATGTTTTGC CCATTGACTA TTACTTTCCA
CCCCTGTACG CAAACCTCTG ACGGTCCCTG GTACAAAACG GGTAACTGAT AATGAAAGGT

      3550        3560        3570        3580        3590        3600
CCCTAGAAGA CCTGCCTGAT CTGTGGAGAT GAAGCTTCTG GGTGTCACTA TGGAGCTCTC
GGGGTCTTCT GGACGGACTA GACACCTCTA CTTCGAAGAC CCACAGTGAT ACCTCGAGAG
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FIGURE 4 (page 5 of 6)

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      3610       3620       3630       3640       3650       3660
ACATGTGGAA GCTGCAAGGT CTTCTTCAAA AGAGCCGCTG AAGGGAAACA GAAGTACCTG
TGTACACCTT CGACGTTCCA GAAGAAGTTT TCTCGGCGAC TTCCCTTTGT CTTCATGGAC

      3670       3680       3690       3700       3710       3720
TGCGCCAGCA GAAATGATTG CACTATTGAT AAATTCCGAA GGAAAAATTG TCCATCTTGT
ACGCGGTCGT CTTTACTAAC GTGATAACTA TTTAAGGCTT CCTTTTTAAC AGGTAGAACA

      3730       3740       3750       3760       3770       3780
CGTCTTCGGA AATGTTATGA AGCAGGGATG ACTCTGGGAG CCCGGAAGCT GAAGAAACTT
GCAGAAGCCT TTACAATACT TCGTCCCTAC TGAGACCCTC GGGCCTTCGA CTTCTTTGAA

      3790       3800       3810       3820       3830       3840
GGTAATCTGA AACTACAGGA GGAAGGAGAG GCTTCCAGCA CCACCAGCCC CACTGAGGAG
CCATTAGACT TTGATGTCCT CCTTCCTCTC CGAAGGTCGT GGTGGTCGGG GTGACTCCTC

      3850       3860       3870       3880       3890       3900
ACAACCCAGA AGCTGACAGT GTCACACATT GAAGGCTATG AATGTCAGCC CATCTTTCTG
TGTTGGGTCT TCGACTGTCA CAGTGTGTAA CTTCCGATAC TTACAGTCGG GTAGAAAGAC

      3910       3920       3930       3940       3950       3960
AATGTCCTGG AAGCCATTGA GCCAGGTGTA GTGTGTGCTG GACACGACAA CAACCAGCCC
TTACAGGACC TTCGGTAACT CGGTCCACAT CACACACGAC CTGTGCTGTT GTTGGTCGGG

      3970       3980       3990       4000       4010       4020
GACTCCTTTG CAGCCTTGCT CTCTAGCCTC AATGAACTGG GAGAGAGACA GCTTGTACAC
CTGAGGAAAC GTCGGAACGA GAGATCGGAG TTACTTGACC CTCTCTCTGT CGAACATGTG

      4030       4040       4050       4060       4070       4080
GTGGTCAAGT GGGCCAAGGG CTTGCCTGGC TTCCGCAACT TACACGTGGA CGACCAGATG
CACCAGTTCA CCCGGTTCCC GAACGGACCG AAGGCGTTGA ATGTGCACCT GCTGGTCTAC

      4090       4100       4110       4120       4130       4140
GCTGTCATTC AGTACTCCTG GATGGGGCTC ATGGTGTTTG CCATGGGCTG GCGATCCTTC
CGACAGTAAG TCATGAGGAC CTACCCCGAG TACCACAAAC GGTACCCGAC CGCTAGGAAG

      4150       4160       4170       4180       4190       4200
ACCAATGTCA ACTCCAGGAT GCTCTACTTC GCCCCTGATC TGGTTTTCAA TGAGTACCGC
TGGTTACAGT TGAGGTCCTA CGAGATGAAG CGGGGACTAG ACCAAAAGTT ACTCATGGCG

      4210       4220       4230       4240       4250       4260
ATGCACAAGT CCCGGATGTA CAGCCAGTGT GTCCGAATGA GGCACCTCTC TCAAGAGTTT
TACGTGTTCA GGGCCTACAT GTCGGTCACA CAGGCTTACT CCGTGGAGAG AGTTCTCAAA

      4270       4280       4290       4300       4310       4320
GGATGGCTCC AAATCACCCC CCAGGAATTC CTGTGCATGA AAGCACTGCT ACTCTTCAGC
CCTACCGAGG TTTAGTGGGG GGTCCTTAAG GACACGTACT TTCGTGACGA TGAGAAGTCG

      4330       4340       4350       4360       4370       4380
ATTATTCCAG TGGATGGGCT GAAAAATCAA AAATTCTTTG ATGAACTTCG AATGAACTAC
TAATAAGGTC ACCTACCCGA CTTTTTAGTT TTTAAGAAAC TACTTGAAGC TTACTTGATG

      4390       4400       4410       4420       4430       4440
ATCAAGGAAC TCGATCGTAT CATTGCATGC AAAAGAAAAA ATCCCACATC CTGCTCAAGA
TAGTTCCTTG AGCTAGCATA GTAACGTACG TTTTCTTTTT TAGGGTGTAG GACGAGTTCT

      4450       4460       4470       4480       4490       4500
CGCTTCTACC AGCTCACCAA GCTCCTGGAC TCCGTGCAGC CTATTGCGAG AGAGCTGCAT
GCGAAGATGG TCGAGTGGTT CGAGGACCTG AGGCACGTCG GATAACGCTC TCTCGACGTA
```

FIGURE 4 (page 6 of 6)

```
      4510        4520        4530        4540        4550        4560
CAGTTCACTT TTGACCTGCT AATCAAGTCA CACATGGTGA GCGTGGACTT TCCGGAAATG
GTCAAGTGAA AACTGGACGA TTAGTTCAGT GTGTACCACT CGCACCTGAA AGGCCTTTAC

      4570        4580        4590        4600        4610        4620
ATGGCAGAGA TCATCTCTGT GCAAGTGCCC AAGATCCTTT CTGGGAAAGT CAAGCCCATC
TACCGTCTCT AGTAGAGACA CGTTCACGGG TTCTAGGAAA GACCCTTTCA GTTCGGGTAG

      4630        4640        4650        4660        4670        4680
TATTTCCACA CCCAGTGAAG CATTGGAAAC CCTATTTCCC CACCCCAGCT CATGCCCCCT
ATAAAGGTGT GGGTCACTTC GTAACCTTTG GGATAAAGGG GTGGGGTCGA GTACGGGGGA

      4690        4700        4710        4720        4730        4740
TTCAGATGTC TTCTGCCTGT TATAACTCTG CACTACTCCT CTGCAGTGCC TTGGGGAATT
AAGTCTACAG AAGACGGACA ATATTGAGAC GTGATGAGGA GACGTCACGG AACCCCTTAA

      4750        4760        4770        4780        4790        4800
TCCTCTATTG ATGTACAGTC TGTCATGAAC ATGTTCCTGA ATTCTATTTG CTGGGCTTTT
AGGAGATAAC TACATGTCAG ACAGTACTTG TACAAGGACT TAAGATAAAC GACCCGAAAA

      4810        4820        4830        4840        4850        4860
TTTTTCTCTT TCTCTCCTTT CTTTTTCTTC TTCCCTCCCT ATCTAACCCT CCCATGGCAC
AAAAAGAGAA AGAGAGGAAA GAAAAAGAAG AAGGGAGGGA TAGATTGGGA GGGTACCGTG

      4870        4880        4890        4900        4910        4920
CTTCAGACTT TGCTTCCCAT TGTGGCTCCT ATCTGTGTTT TGAATGGTGT TGTATGCCTT
GAAGTCTGAA ACGAAGGGTA ACACCGAGGA TAGACACAAA ACTTACCACA ACATACGGAA

      4930        4940        4950        4960        4970        4980
TAAATCTGTG ATGATCCTCA TATGGCCCAG TGTCAAGTTG TGCTTGTTTA CAGCACTACT
ATTTAGACAC TACTAGGAGT ATACCGGGTC ACAGTTCAAC ACGAACAAAT GTCGTGATGA

      4990        5000        5010        5020        5030        5040
CTGTGCCAGC CACACAAACG TTTACTTATC TTATGCCACG GGAAGTTTAG AGAGCTAAGA
GACACGGTCG GTGTGTTTGC AAATGAATAG AATACGGTGC CCTTCAAATC TCTCGATTCT

      5050        5060        5070        5080
TTATCTGGGG AAATCAAAAC AAAAAACAAG CAAACAAAAA AAAAA
AATAGACCCC TTTAGTTTTG TTTTTTGTTC GTTTGTTTTT TTTTT
```

FIGURE 5 (page 1 of 5)

```
        10         20         30         40         50         60
GAGCTCTGGA CAAAATTGAG CGCCTATGTG TACATGGCAA GTGTTTTTAG TGTTTGTGTG

        70         80         90        100        110        120
TTTACCTGCT TGTCTGGGTG ATTTTGCCTT TGAGAGTCTG GATGAGAAAT GCATGGTTAA

       130        140        150        160        170        180
AGGCAATTCC AGACAGGAAG AAAGGCAGAG AAGAGGGTAG AAATGACCTC TGATTCTTGG

       190        200        210        220        230        240
GGCTGAGGGT TCCTAGAGCA AATGGCACAA TGCCACGAGG CCCGATCTAT CCCTATGACG

       250        260        270        280        290        300
GAACTCTAAG GTTTCAGCAT CAGCTATCTG CTGGCTTGGT CACTGGCTTG CCTCCTCAGT

       310        320        330        340        350        360
TTGTAGGAGA CTCTCCCACT CTCCCATCTG CGCGCTCTTA TCAGTCCTGA AAAGAACCCN

       370        380        390        400        410        420
TGGCNAGCCA GGAGCNAGGT ATTCNTATCG TCCTTTTCNT CCTCCTNGCC TCACCTNGTT

       430        440        450        460        470        480
GNTTTTTAGA TTGGNCTTNG NAACCAAATT TGTATGCTGG CCTCCAGGAA ATCTGGAGCC

       490        500        510        520        530        540
TGGCGCCTAA ACCTTGGTTT AGGAAAGCAG GAGCTATTCA GGAAGCAGGG TCCTCCAGGG

       550        560        570        580        590        600
CTAGAGCTAG CCTCTCCTGC CCTCGCCCAC GTGCGCCAGC ACTTGTTTCT CCAAAGCNAC

       610        620        630        640        650        660
TAGGCAGGCG TTAGCGCGCG GTGAGGGGAG GGGAGAAAAG GAAAGGGGAG GGGAGGGAAA

       670        680        690        700        710        720
AGGAGGTGGG AAGGCAAGGA GGCCGGCCNG GTGGGGGCGG GACCCGACTC GCANNAACTG

       730        740        750        760        770        780
TTGCATTTGC TCTCCACCTC CCAGCGCCCC CTCCGAGATC CCGGGGAGCC AGCTTGCTGG

       790        800        810        820        830        840
GAGAGCGGGA ACGGTCCGGA GCAAGCCCAG AGGCAGAGGA GGCGACAGAG GGAAAAAGGG

       850        860        870        880        890        900
CCCNAGCTAG CCGCTCCAGT GCTGTACAGN AGCCGAAGGA CGCACCACGC CAGCCCCAGC

       910        920        930        940        950        960
CCGGCTCCAG CGACAGCNAA CGCCTCTTGC ANGCGTTCGA AGCCGCCGCC CGGAGCTGCC

       970        980        990       1000       1010       1020
CTTTCCTCTT CGGTGAAGTT TTTAAAAGCT GCTAAAGACT CGGAGGAAGC AAGGAAAGTG

      1030       1040       1050       1060       1070       1080
CCTGGTAGGA CTGACGGCTG CCTTTGTCCT CCTCCTCTCC ACCCCGCCTC CCCCCACCCT

      1090       1100       1110       1120       1130       1140
GCCTTCCCCC CCTCCCCCGT CTTCTCTCCC GCAGCTGCCT CAGTCGGCTA CTCTCAGCCA

      1150       1160       1170       1180       1190       1200
ACCCCCCTCA CCACCCTTCT CCCCACCCGC CCCCCCGCCC CCGTCGGCCC AGCGNTGNCA

      1210       1220       1230       1240       1250       1260
GNCCGAGTTT GCAGAGAGGT AACTCCCTTT AGCTGCGAGC GGGCGAGNCT AGCTGCACAT
```

FIGURE 5 (page 2 of 5)

```
      1270        1280        1290        1300        1310        1320
TGCAAAGAAG GCTCTTAGGA GCAGGCGACT GGGGAGCGGC TTCAGCACTG CAGCCACGAC

      1330        1340        1350        1360        1370        1380
CNGCCTGGTT AGGCTGCACG CGGAGAGAAC CCTCTGTTTT CCCCCACTCT CTCTCCACCT

      1390        1400        1410        1420        1430        1440
CCTCCTGCCT TCCCCACCCC GAGTGCGGAG CCAGAGATCA AAAGATGAAA AGGCAGTCAG

      1450        1460        1470        1480        1490        1500
GTCTTCAGTA GCCAAAAAAC AAAACAAACA AAAACAAAAA AGCCGAAATA AAAGAAAAAG

      1510        1520        1530        1540        1550        1560
ATAATAACTC AGTTCTTATT TGCACCTACT TCAGTGGACA CTGAATTTGG AAGGTGGAGG

      1570        1580        1590        1600        1610        1620
ATTTTGTTTT TTTCTTTTAA GATCTGGGCA TCTTTTGAAT CTACCCTTCA AGTATTAAGA

      1630        1640        1650        1660        1670        1680
GACAGACTGT GAGCCTAGCA GGGCAGATCT TGTCCACCGT GTGTCTTCTT CTGCACGAGA

      1690        1700        1710        1720        1730        1740
CTTTGAGGCT GTCAGAGCGC TTTTTGCGTG GTTGCTCCCG CAAGTTTCCT TCTCTGGAGC

      1750        1760        1770        1780        1790        1800
TTCCCGCAGG TGGGCAGCTA GCTGCAGCGA CTACCGCATC ATCACAGCCT GTTGAACTCT

      1810        1820        1830        1840        1850        1860
TCTGAGCAAG AGAAGGGGAG GCGGGGTAAG GGAAGTAGGT GGAAGATTCA GCCAAGCTCA

                                  1890                                1920
65G ATG GAA GTG CAG TTA GGG CTG GGA AGG GTC TAC CCT CGG CCG CCG TCC AAG ACC T-C
    Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser Lys Thr Tyr

                                  1950                                1980
CGA GGA GCT TTC CAG AAT CTG TTC CAG AGC GTG CGC GAA GTG ATC CAG AAC CCG GGC CCC
Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu Val Ile Gln Asn Pro Gly Pro

                                  2010                                2040
AGG CAC CCA GAG GCC GCG AGC GCA GCC CCT CCC GGC GCC AGT TTG CTG CTG CTG CAG CAG
Arg His Pro Glu Ala Ala Ser Ala Ala Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln

                                  2070                                2100
CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln

                                  2130                                2160
CAG CAG CAA GAG ACT AGC CCC AGG CAG CAG CAG CAG CAG CAG GGT GAG GAT GGT TCT CCC
Gln Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro

                                  2190                                2220
CAA GCC CAT CGT AGA GGC CCC ACA GGC TAC CTG GTC CTG GAT GAG GAA CAG CAA CCT TCA
Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln Gln Pro Ser

                                  2250                                2280
CAG CCG CAG TCG GCC CTG GAG TGC CAC CCC GAG AGA GGT TGC GTC CCA GAG CCT GGA GCC
Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala

                                  2310                                2340
GCC GTG GCC GCC AGC AAG GGG CTG CCG CAG CAG CTG CCA GCA CCT CCG GAC GAG GAT GAC
Ala Val Ala Ala Ser Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp
```

FIGURE 5 (page 3 of 5)

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                                                                2370                                                                2400
TCA GCT GCC CCA TCC ACG TTG TCC CTG CTG GGC CCC ACT TTC CCC GGC TTA AGC AGC TGC
Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys

                                                                2430                                                                2460
TCC GCT GAC CTT AAA GAC ATC CTG AGC GAG GCC AGC ACC ATG CAA CTC CTT CAG CAA CAG
Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu Gln Gln Gln

                                                                2490                                                                2520
CAG CAG GAA GCA GTA TCC GAG GGC AGC AGC AGC GGG AGA GCG AGG GAG GCC TCG GGG GCT
Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala

                                                                2550                                                                2580
CCC ACT TCC TCC AAG GAC AAT TAC TTA GGG GGC ACT TCG ACC ATT TCT GAC AAC GCC AAG
Pro Thr Ser Ser Lys Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys

                                                                2610                                                                2640
GAG CTG TGT AAG GCA GTG TCG GTG TCC ATG GGC CTG GGT GTG GAG GCG TTG GAG CAT CTG
Glu Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu

                                                                2670                                                                2700
AGT CCA GGG GAA CAG CTT CGG GGG GAT TGC ATG TAC GCC CCA CTT TTG GGA GTT CCA CCC
Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly Val Pro Pro

                                                                2730                                                                2760
GCT GTG GCT CCC ACT CCT TGT GCC CCA TTG GCC GAA TGC AAA GGT TCT CTG CTA GAC GAC
Ala Val Ala Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp

                                                                2790                                                                2820
AGC GCA GGC AAG AGC ACT GAA GAT ACT GCT GAG TAT TCC CCT TTC AAG GGA GGT TAC ACC
Ser Ala Gly Lys Ser Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr

                                                                2850                                                                2880
AAA GGG CTA GAA GGC GAG AGC CTA GGC TGC TCT GGC AGC GCT GCA GCA GGG AGC TCC GGG
Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly

                                                                2910                                                                2940
ACC CTT GAA CTG CCG TCT ACC CTG TCT CTC TAC AAG TCC GGA GCA CTG GAC GAG GCA GCT
Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala

                                                                2970                                                                3000
GCG TAC CAG AGT CGC GAC TAC TAC AAC TTT CCA CTG GCT CTG GCC GGA CCG CCG CCC CCT
Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro

                                                                3030                                                                3060
CCG CCG CCT CCC CAT CCC CAC GCT CGC ATC AAG CTG GAG AAC CCG CTG GAC TAC GGC AGC
Pro Pro Pro Pro His Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser

                                                                3090                                                                3120
GCC TGG GCG GCT GCG GCG GCG CAG TGC CGC TAT GGG GAC CTG GCG AGC CTG CAT GGC GCG
Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala

                                                                3150                                                                3180
GGT GCA GCG GGA CCC GGT TCT GGG TCA CCC TCA GCC GCC GCT TCC TCA TCC TGG CAC ACT
Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser Trp His Thr

                                                                3210                                                                3240
CTC TTC ACA GCC GAA GAA GGC CAG TTG TAT GGA CCG TGT GGT GGT GGT GGG GGT GGT GGC
Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys Gly Gly Gly Gly Gly Gly Gly
```

FIGURE 5 (page 4 of 5)

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                                                3270                                                3300
GGC GGC GGC GGC GGC GGC GGC GGC GGC GGC GGC GGC GGC GGC GGC GGC GGC GAG GCG GGA
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly

                                                3330                                                3360
GCT GTA GCC CCC TAC GGC TAC ACT CGG CCC CCT CAG GGG CTG GCG GGC CAG GAA AGC GAC
Ala Val Ala Pro Tyr Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp

                                                3390                                                3420
TTC ACC GCA CCT GAT GTG TGG TAC CCT GGC GGC ATG GTG AGC AGA GTG CCC TAT CCC AGT
Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro Tyr Pro Ser

                                                3450                                                3480
CCC ACT TGT GTC AAA AGC GAA ATG GGC CCC TGG ATG GAT AGC TAC TCC CGG GAA CCT TAC
Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp Ser Tyr Ser Arg Glu Pro Tyr

                                                3510                                                3540
GGG GAC ATG CGT TTG GAG ACT GCC AGG GAC CAT GTT TTG CCC ATT GAC TAT TAC TTT CCA
Gly Asp Met Arg Leu Glu Thr Ala Arg Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro

                                                3570                                                3600
CCC CAG AAG ACC TGC CTG ATC TGT GGA GAT GAA GCT TCT GGG TGT CAC TAT GGA GCT CTC
Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu

                                                3630                                                3660
ACA TGT GGA AGC TGC AAG GTC TTC TTC AAA AGA GCC GCT GAA GGG AAA CAG AAG TAC CTG
Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu

                                                3690                                                3720
TGC GCC AGC AGA AAT GAT TGC ACT ATT GAT AAA TTC CGA AGG AAA AAT TGT CCA TCT TGT
Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys

                                                3750                                                3780
CGT CTT CGG AAA TGT TAT GAA GCA GGG ATG ACT CTG GGA GCC CGG AAG CTG AAG AAA CTT
Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu

                                                3810                                                3840
GGT AAT CTG AAA CTA CAG GAG GAA GGA GAG GCT TCC AGC ACC ACC AGC CCC ACT GAG GAG
Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu

                                                3870                                                3900
ACA ACC CAG AAG CTG ACA GTG TCA CAC ATT GAA GGC TAT GAA TGT CAG CCC ATC TTT CTG
Thr Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu

                                                3930                                                3960
AAT GTC CTG GAA GCC ATT GAG CCA GGT GTA GTG TGT GCT GGA CAC GAC AAC AAC CAG CCC
Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn Gln Pro

                                                3990                                                4020
GAC TCC TTT GCA GCC TTG CTC TCT AGC CTC AAT GAA CTG GGA GAG AGA CAG CTT GTA CAC
Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His

                                                4050                                                4080
GTG GTC AAG TGG GCC AAG GGC TTG CCT GGC TTC CGC AAC TTA CAC GTG GAC GAC CAG ATG
Val Val Lys Trp Ala Lys Gly Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met

                                                4110                                                4140
GCT GTC ATT CAG TAC TCC TGG ATG GGG CTC ATG GTG TTT GCC ATG GGC TGG CGA TCC TTC
Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe
```

FIGURE 5 (page 5 of 5)

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                                         4170                                    4200
ACC AAT GTC AAC TCC AGG ATG CTC TAC TTC GCC CCT GAT CTG GTT TTC AAT GAG TAC CGC
Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg

                                         4230                                    4260
ATG CAC AAG TCC CGG ATG TAC AGC CAG TGT GTC CGA ATG AGG CAC CTC TCT CAA GAG TTT
Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe

                                         4290                                    4320
GGA TGG CTC CAA ATC ACC CCC CAG GAA TTC CTG TGC ATG AAA GCA CTG CTA CTC TTC AGC
Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser

                                         4350                                    4380
ATT ATT CCA GTG GAT GGG CTG AAA AAT CAA AAA TTC TTT GAT GAA CTT CGA ATG AAC TAC
Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr

                                         4410                                    4440
ATC AAG GAA CTC GAT CGT ATC ATT GCA TGC AAA AGA AAA AAT CCC ACA TCC TGC TCA AGA
Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg

                                         4470                                    4500
CGC TTC TAC CAG CTC ACC AAG CTC CTG GAC TCC GTG CAG CCT ATT GCG AGA GAG CTG CAT
Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His

                                         4530                                    4560
CAG TTC ACT TTT GAC CTG CTA ATC AAG TCA CAC ATG GTG AGC GTG GAC TTT CCG GAA ATG
Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met

                                         4590                                    4620
ATG GCA GAG ATC ATC TCT GTG CAA GTG CCC AAG ATC CTT TCT GGG AAA GTC AAG CCC ATC
Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile

                                         4650                                    4680
TAT TTC CAC ACC CAG TGA AGC ATT GGA AAC CCT ATT TCC CCA CCC CAG CTC ATG CCC CCT
Tyr Phe His Thr Gln End

      4690       4700       4710       4720       4730       4740
TTCAGATGTC TTCTGCCTGT TATAACTCTG CACTACTCCT CTGCAGTGCC TTGGGGAATT

      4750       4760       4770       4780       4790       4800
TCCTCTATTG ATGTACAGTC TGTCATGAAC ATGTTCCTGA ATTCTATTTG CTGGGCTTTT

      4810       4820       4830       4840       4850       4860
TTTTTCTCTT TCTCTCCTTT CTTTTTCTTC TTCCCTCCCT ATCTAACCCT CCCATGGCAC

      4870       4880       4890       4900       4910       4920
CTTCAGACTT TGCTTCCCAT TGTGGCTCCT ATCTGTGTTT TGAATGGTGT TGTATGCCTT

      4930       4940       4950       4960       4970       4980
TAAATCTGTG ATGATCCTCA TATGGCCCAG TGTCAAGTTG TGCTTGTTTA CAGCACTACT

      4990       5000       5010       5020       5030       5040
CTGTGCCAGC CACACAAACG TTTACTTATC TTATGCCACG GGAAGTTTAG AGAGCTAAGA

      5050       5060       5070       5080
TTATCTGGGG AAATCAAAAC AAAAAACAAG CAAACAAAAA AAAAA
```

FIGURE 6 (page 1 of 5)

F1 1

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        10        20        30        40        50        60
AATTCGGGAAGGATCGAGCAAACCAGGAAAGTAAGGATGGAGATCCTAGGAGAGTGTCCA

        70        80        90       100       110       120
TGCCTCGAAAGGAGCCCACCAAAGATGAACTGTTGCATTTGCTTTCCACCTCCCAGCGCC

       130       140       150       160       170       180
CCCTCGGAGATCCCTAGGAGCCAGCCTGCTGGGAGAACCAGAGGGTCCGGAGCAAACCTG

       190       200       210       220       230       240
GAGGCTGAGAGGGCATCAGAGGGGAAAAGACTGAGTTAGCCACTCCAGTGCCATACAGAA

       250       260       270       280       290       300
GCTTAAGGGACATACCACGCCAGCCCCAGCCCAGCGACAGCCAACGCCTGTTGCAGAGCG

       310       320       330       340       350       360
GCGGCTTCGAAGCCGCCGCCCAGAAGCTGCCCTTTCCTCTTCGGTGAAGTTTCTAAAAGC

       370       380       390       400       410       420
TGCGGGAGACTCGGAGGAAGCGAAGAAAGTGTCCGGTAGGACTACGACTGCCTTTGTCCT

       430       440       450       460       470       480
CCTCCCTCCTACCCCTACCCCTCCTGGGTCCCCTCTCCCTGAGCGGACTAGGCAGGCTTC

       490       500       510       520       530       540
CTGGCCAGCCCTCTCCCCTACACCACCAGCTCTGCCAGCCAGTTTGCACAGAGGTAACTC

       550       560       570       580       590       600
CCTTTGGCTGAAAGCAGACGAGCTTGTTGCCCATTGGAAGGGAGGCTTTTGGGAGCCCAG

       610       620       630       640       650       660
AGACTGAGGAGCAACAGCACGCTGGAGAGTCCCTGATTCCAGGTTCTCCCCCCTGCACCT

       670       680       690       700       710       720
CCTACTGCCCGCCCCTCACCCTGTGTGTGCAGCTAGAATTGAAAAGATGAAAAGACAGTT

       730       740       750       760       770       780
GGGGCTTCAGTAGTCGAAAGCAAAACAAAAGCAAAAAGAAAACAAAAAGAAAATAGCCCA

       790       800       810       820       830       840
GTTCTTATTTGCACCTGCTTCAGTGGACATTGACTTTGGAAGGCAGAGAATTTTCCTTCC

       850       860       870       880       890       900
CCCCAGTCAAGCTTTGAGCATCTTTTAATCTGTTCTTCAAGTATTTAGGGACAAACTGTG
```

FIGURE 6 (page 2 of 5)

1 1

```
       910       920       930       940       950       960
AAACTAGCAGGGCAGATCCTGTCTAGCGCGTGCCTTCCTTTACAGGAGACTTTGAGGCTA

       970       980       990      1000      1010      1020
TCTGGGCGCTCCCCCCCCTCCCTGCAAGTTTTCTTCCCTGGAGCTTCCCGCAGGTGGGCA

      1030      1040      1050      1060      1070      1080
GCTAGCTGCAGATACTACATCATCAGTCAGTAGAACTCTTCAGAGCAAGAGACGAGGAGG

      1090      1100      1110      1120      1130      1140
CAGGATAAGGGAATTCGGTGGAAGCTAGAGACAAGCTAAAGGATGGAGGTGCAGTTAGGG
                                          MetGluValGlnLeuGly

      1150      1160      1170      1180      1190      1200
CTGGGAAGGGTCTACCCACGGCCCCCGTCCAAGACCTATCGAGGAGCGTTCCAGAATCTG
LeuGlyArgValTyrProArgProProSerLysThrTyrArgGlyAlaPheGlnAsnLeu

      1210      1220      1230      1240      1250      1260
TTCCAGAGCGTGCGCGAAGCGATCCAGAACCCGGGCCCCAGGCACCCTGAGGCCGCTAGC
PheGlnSerValArgGluAlaIleGlnAsnProGlyProArgHisProGluAlaAlaSer

      1270      1280      1290      1300      1310      1320
ATAGCACCTCCCGGTGCCTGTTTACAGCAGCGGCAGGAGACTAGCCCCCGGCGGCGGCGG
IleAlaProProGlyAlaCysLeuGlnGlnArgGlnGluThrSerProArgArgArgArg

      1330      1340      1350      1360      1370      1380
CGGCAGCAGCACCCTGAGGATGGCTCTCCTCAAGCCCACATCAGAGGCACCACAGGCTAC
ArgGlnGlnHisProGluAspGlySerProGlnAlaHisIleArgGlyThrThrGlyTyr

      1390      1400      1410      1420      1430      1440
CTGGCCCTGGAGGAGGAACAGCAGCCTTCACAGCAGCAGTCAGCCTCCGAGGGCCACCCT
LeuAlaLeuGluGluGluGlnGlnProSerGlnGlnGlnSerAlaSerGluGlyHisPro

      1450      1460      1470      1480      1490      1500
GAGAGCGGCTGCCTCCCGGAGCCTGGAGCTGCCACGGCTCCTGGCAAGGGGCTGCCGCAG
GluSerGlyCysLeuProGluProGlyAlaAlaThrAlaProGlyLysGlyLeuProGln

      1510      1520      1530      1540      1550      1560
CAGCCACCAGCTCCTCCAGATCAGGATGACTCAGCTGCCCCATCCACGTTGTCCCTACTG
GlnProProAlaProProAspGlnAspAspSerAlaAlaProSerThrLeuSerLeuLeu

      1570      1580      1590      1600      1610      1620
GGCCCCACTTTCCCAGGCTTAAGCAGCTGCTCCGCAGACATTAAAGACATCCTGAGCGAG
GlyProThrPheProGlyLeuSerSerCysSerAlaAspIleLysAspIleLeuSerGlu

      1630      1640      1650      1660      1670      1680
GCCGGCACCATGCAACTTCTTCAGCAGCAGCAGCAACAGCAACAGCAGCAGCAGCAGCAG
AlaGlyThrMetGlnLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln

      1690      1700      1710      1720      1730      1740
CAGCAGCAGCAGCAGCAACAGCAGCAGGAGGTAATATCCGAAGGCAGCAGCAGCGTGAGA
GlnGlnGlnGlnGlnGlnGlnGlnGlnGluValIleSerGluGlySerSerSerValArg

      1750      1760      1770      1780      1790      1800
GCAAGGGAGGCCACTGGGGCTCCCTCTTCCTCCAAGGATAG TACCTAGGGGGCAATTCG
AlaArgGluAlaThrGlyAlaProSerSerSerLysAspSerTyrLeuGlyGlyAsnSer
```

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       1910      1820      1830      1840      1850      1860
ACCATATCTGACAGTGCCAAGGAGTTGTGTAAAGCAGTGTCTGTGTCCATGGGGTTGGGT
ThrIleSerAspSerAlaLysGluLeuCysLysAlaValSerValSerMetGlyLeuGly

       1870      1880      1890      1900      1910      1920
GTGGAAGCACTGGAACATCTGAGTCCAGGGGAGCAGCTTCGGGGCGACTGCATGTACGCG
ValGluAlaLeuGluHisLeuSerProGlyGluGlnLeuArgGlyAspCysMetTyrAla

       1930      1940      1950      1960      1970      1920
TCGCTCCTGGGAGGTCCACCCGCCGTGCGTCCCACTCCTTGTGCGCCTCTGGCCGAATGC
SerLeuLeuGlyGlyProProAlaValArgProThrProCysAlaProLeuAlaGluCys

       1990      2000      2010      2020      2030      2040
AAAGGTCTTTCCCTGGACGAAGGCCCGGGCAAAGGCACTGAAGAGACTGCTGAGTATTCC
LysGlyLeuSerLeuAspGluGlyProGlyLysGlyThrGluGluThrAlaGluTyrSer

       2050      2060      2070      2080      2090      2100
TCTTTCAAGGGAGGTTACGCCAAAGGGTTGGAAGGTGAGAGTCTGGGCTGCTCTGGCAGC
SerPheLysGlyGlyTyrAlaLysGlyLeuGluGlyGluSerLeuGlyCysSerGlySer

       2110      2120      2130      2140      2150      2160
AGTGAAGCAGGTAGCTCTGGGACACTTGAGATCCCGTCCTCACTGTCTCTGTATAAGTCT
SerGluAlaGlySerSerGlyThrLeuGluIleProSerSerLeuSerLeuTyrLysSer

       2170      2180      2190      2200      2210      2220
GGAGCAGTAGACGAGGCAGCAGCATACCAGAATCGCGACTACTACAACTTTCCGCTCGCT
GlyAlaValAspGluAlaAlaAlaTyrGlnAsnArgAspTyrTyrAsnPheProLeuAla

       2230      2240      2250      2260      2270      2280
CTGTCCGGGCCGCCGCACCCCCCGCCCCCTACCCATCCACACGCCCGCATCAAGCTGGAG
LeuSerGlyProProHisProProProProThrHisProHisAlaArgIleLysLeuGlu

       2290      2300      2310      2320      2330      2340
AACCCGTCGGACTACGGCAGCGCCTGGGCTGCGGCGGCAGCGCAATGCCGCTATGGGGAC
AsnProSerAspTyrGlySerAlaTrpAlaAlaAlaAlaAlaGlnCysArgTyrGlyAsp

       2350      2360      2370      2320      2390      2400
TTGGCTAGCCTACATGGAGGGAGTGTAGCCGGACCCAGCACTGGATCGCCCCCAGCCACC
LeuAlaSerLeuHisGlyGlySerValAlaGlyProSerThrGlySerProProAlaThr

       2410      2420      2430      2440      2450      2460
GCCTCTTCTTCCTGGCATACTCTCTTCACAGCTGAAGAAGGCCAATTATATGGGCCAGGA
AlaSerSerSerTrpHisThrLeuPheThrAlaGluGluGlyGlnLeuTyrGlyProGly

       2470      2480      2450      2500      2510      2520
GGCGGGGGCGGCAGCAGTAGCCCAAGCGATGCTGGGCCTGTAGCCCCCTATGGCTACACT
GlyGlyGlyGlySerSerSerProSerAspAlaGlyProValAlaProTyrGlyTyrThr

       2530      2540      2550      2560      2570      2590
CGGCCCCCTCAGGGGCTGGCAAGCCAGGAGGGTGACTTCTCTGCCTCTGAAGTGTGGTAT
ArgProProGlnGlyLeuAlaSerGlnGluGlyAspPheSerAlaSerGluValTrpTyr

       2590      2600      2610      2620      2630      2640
CCTGGTGGAGTTGTGAACAGAGTCCCCTATCCCAGTCCCAGTTGTGTTAAAAGTGAAATG
ProGlyGlyValValAsnArgValProTyrProSerProSerCysValLysSerGluMet

       2650      2660      2670      2680      2690      2700
GGACCTTGGATGGAGAACTACTCCGGACCTTATGGGGACATGCGTTTGGACAGTACCAGG
GlyProTrpMetGluAsnTyrSerGlyProTyrGlyAspMetArgLeuAspSerThrArg
```

FIGURE 6 (page 4 of 5)

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      2710        2720        2730        2740        2750        2760
GACCACGTTTTACCCATCGACTATTACTTCCCACCCCAGAAGACCTCCCTGATCTGTGGA
AspHisValLeuProIleAspTyrTyrPheProProGlnLysThrCysLeuIleCysGly

      2770        2780        2790        2800        2810        2820
GATGAAGCTTCTGGTTGTCACTACGGAGCTCTCACTTGTGGCAGCTGCAAGGTCTTCTTC
AspGluAlaSerGlyCysHisTyrGlyAlaLeuThrCysGlySerCysLysValPhePhe

      2830        2840        2850        2860        2870        2880
AAAAGAGCTGCGGAAGGGAAACAGAAGTATCTATGTGCCAGCAGAAATGATTGCACCATT
LysArgAlaAlaGluGlyLysGlnLysTyrLeuCysAlaSerArgAsnAspCysThrIle

      2890        2900        2910        2920        2930        2940
GATAAATTTCGGAGGAAAAATTGTCCATCGTGTCGTCTCCGGAAATGTTATGAAGCAGGG
AspLysPheArgArgLysAsnCysProSerCysArgLeuArgLysCysTyrGluAlaGly

      2950        2960        2970        2980        2990        3000
ATGACTCTGGGAGCTCGTAAGCTGAAGAAACTTGGAAATCTCAAACTACAGGAAGAAGGA
MetThrLeuGlyAlaArgLysLeuLysLysLeuGlyAsnLeuLysLeuGlnGluGluGly

      3010        3020        3030        3040        3050        3060
GAAAACTCCAGTGCTGGTAGCCCCACTGAGGACCCATCCCAGAAGATGACTGTATCACAC
GluAsnSerSerAlaGlySerProThrGluAspProSerGlnLysMetThrValSerHis

      3070        3080        3090        3100        3110        3120
ATTGAAGGCTATGAATGTCAACCTATCTTTCTTAATGTCCTGGAAGCCATTGAGCCAGGA
IleGluGlyTyrGluCysGlnProIlePheLeuAsnValLeuGluAlaIleGluProGly

      3130        3140        3150        3160        3170        3180
GTGGTGTGTGCCGGACATGACAACAACCAGCCTGATTCCTTTGCTGCCTTGTTATCTAGT
ValValCysAlaGlyHisAspAsnAsnGlnProAspSerPheAlaAlaLeuLeuSerSer

      3190        3200        3210        3220        3230        3240
CTCAACGAGCTTGGCGAGAGACAGCTTGTACATGTGGTCAAGTGGGCCAAGGCCTTGCCT
LeuAsnGluLeuGlyGluArgGlnLeuValHisValValLysTrpAlaLysAlaLeuPro

      3250        3260        3270        3280        3290        3300
GGCTTCCGCAACTTGCATGTGGATGACCAGATGGCAGTCATTCAGTATTCCTGGATGGGA
GlyPheArgAsnLeuHisValAspAspGlnMetAlaValIleGlnTyrSerTrpMetGly

      3310        3320        3330        3340        3350        3360
CTGATGGTATTTGCCATGGGTTGGCGGTCCTTCACTAATGTCAACTCTAGGATGCTCTAC
LeuMetValPheAlaMetGlyTrpArgSerPheThrAsnValAsnSerArgMetLeuTyr

      3370        3380        3390        3400        3410        3420
TTTGCACCTGACCTGGTTTTCAATGAGTATCGCATGCACAAGTCTCGAATGTACAGCCAG
PheAlaProAspLeuValPheAsnGluTyrArgMetHisLysSerArgMetTyrSerGln

      3430        3440        3450        3460        3470        3480
TGCGTGAGGATGAGGCACCTTTCTCAAGAGTTTGGATGGCTCCAGATAACCCCCCAGGAA
CysValArgMetArgHisLeuSerGlnGluPheGlyTrpLeuGlnIleThrProGlnGlu

      3490        3500        3510        3520        3530        3540
TTCCTGTGCATGAAAGCACTGCTACTCTTCAGCATTATTCCAGTGGATGGGCTGAAAAAT
PheLeuCysMetLysAlaLeuLeuLeuPheSerIleIleProValAspGlyLeuLysAsn

      3550        3560        3570        3580        3590        3600
CAAAAATTCTTTGATGAACTTCGAATGAACTACATCAAGGAACTTGATCGCATCATTGCA
GlnLysPhePheAspGluLeuArgMetAsnTyrIleLysGluLeuAspArgIleIleAla
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FIGURE 6 (page 5 of 5)

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      3610        3620        3630        3640        3650        3660
TGCAAAAGAAAAAATCCCACATCCTGCTCAAGGCGCTTCTACCAGCTCACCAAGCTCCTG
CysLysArgLysAsnProThrSerCysSerArgArgPheTyrGlnLeuThrLysLeuLeu

      3670        3680        3690        3700        3710        3720
GATTCTGTGCAGCCTATTGCAAGAGAGCTGCATCAATTCACTTTTGACCTGCTAATCAAG
AspSerValGlnProIleAlaArgGluLeuHisGlnPheThrPheAspLeuLeuIleLys

      3730        3740        3750        3760        3770        3780
TCCCATATGGTGAGCGTGGACTTTCCTGAAATGATGGCAGAGATCATCTCTGTGCAAGTG
SerHisMetValSerValAspPheProGluMetMetAlaGluIleIleSerValGlnVal

      3790        3800        3810        3820        3830        3840
CCCAAGATCCTTTCTGGGAAAGTCAGCCCATGTATTTCCACACACAGTGAAGATTTGGAA
ProLysIleLeuSerGlyLysValSerProCysIleSerThrHisSerGluAspLeuGlu

      3850        3860        3870        3880        3890        3900
CCTAATACCCAAACCCACCTGTTCCCTTTTCAGATGTCTTCTGCCTGTTATATAACTCTG
ProAsnThrGlnThrHisLeuPheProPheGlnMetSerSerAlaCysTyrIleThrLeu

      3910        3920        3930        3940        3950        3960
CACTACTTCTCTGGCATGGGCCTTGGGGGAAATTCCTCTACTGATGTACAGTCTGTCATG
HisTyrPheSerGlyMetGlyLeuGlyGlyAsnSerSerThrAspValGlnSerValMet

      3970        3980        3990        4000        4010        4020
AACATGTTCCCCAAGTTCTATTTCCTGGGCTTTTCCTTCTTTCTTTTTCTTCTTCTCTGC
AsnMetPheProLysPheTyrPheLeuGlyPheSerPhePheLeuPheLeuLeuLeuCys

      4030        4040        4050        4060        4070        4080
CTCTTTTACCCTCCCATGGCACATTTTGAATCCGCTGCGTGTTGTGGCTCCTGCCTGTGT
LeuPheTyrProProMetAlaHisPheGluSerAlaAlaCysCysGlySerCysLeuCys

      4090        4100        4110        4120        4130        4140
TTTGAGTTTTGTTGTATTTCTTCAAGTCTGTGATGATCTTCTTGTGGCCCAGTGTCAACT
PheGluPheCysCysIleSerSerSerLeuEnd

      4150        4160        4170        4180        4190        4200
GTGCTTGTTTATAGCACTGTGCTGTGTGCCAACCAAGCAAATGTTTACTCACCTTATGCC

      4210        4220        4230        4240        4250        4260
ATGGCAAGTTTAGAGAGCTATAAGTATCTTGGGAAGAAACAAACAGAGAGAGTAAAAAAA

      4270        4280
CCAAAAAAAAAAAAAAAAAAGCCGAATTC
```

FIGURE 7

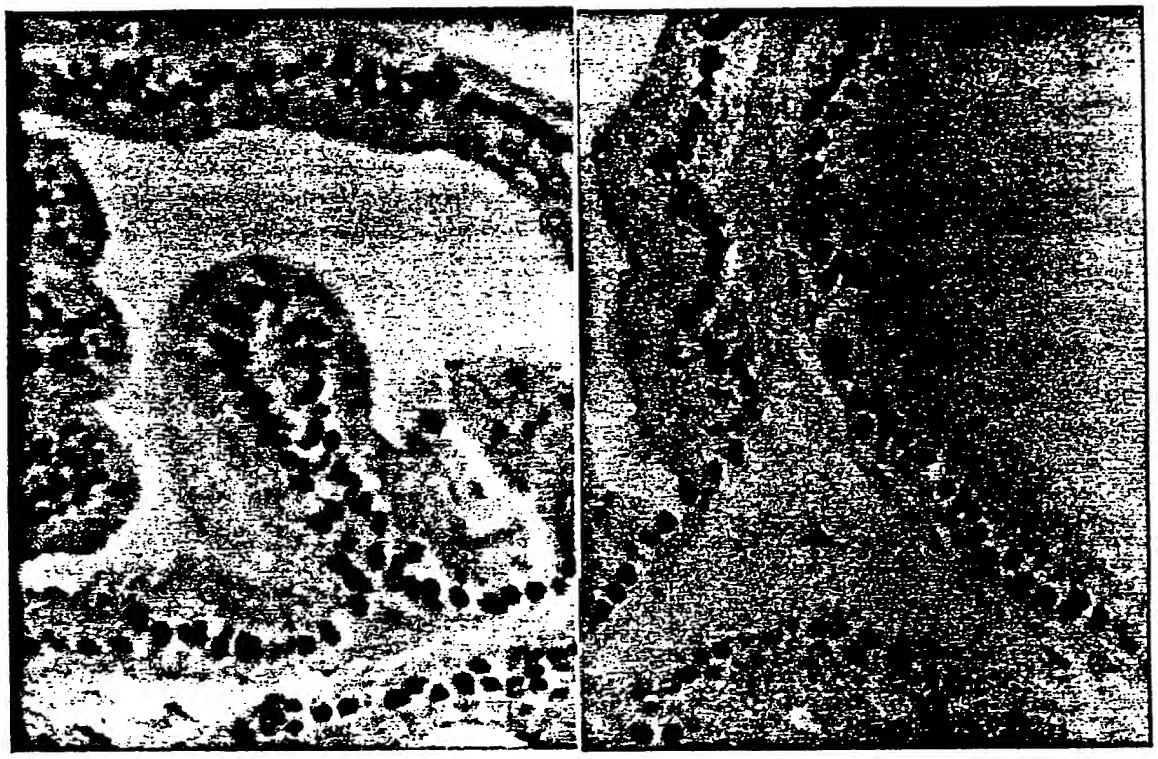

Figure 7 . Frozen section of rat ventral prostate stained with antibodies (AR-52-3-p) to the AR peptide NH_2-Asp-His-Val-Leu-Pro-Ile-Asp-Tyr-Tyr-Phe-Pro-Pro-Gln-Lys-Thr in a dilution of 1 to 3000 using the avidin-biotin peroxidase technique. Androgen receptor is indicated by brown staining of nuclei in epithelial cells. Immuno-staining was performed as previously described (60).

FIGURE 8

Restriction Fragment Length Polymorphism in the Human Androgen Receptor Gene

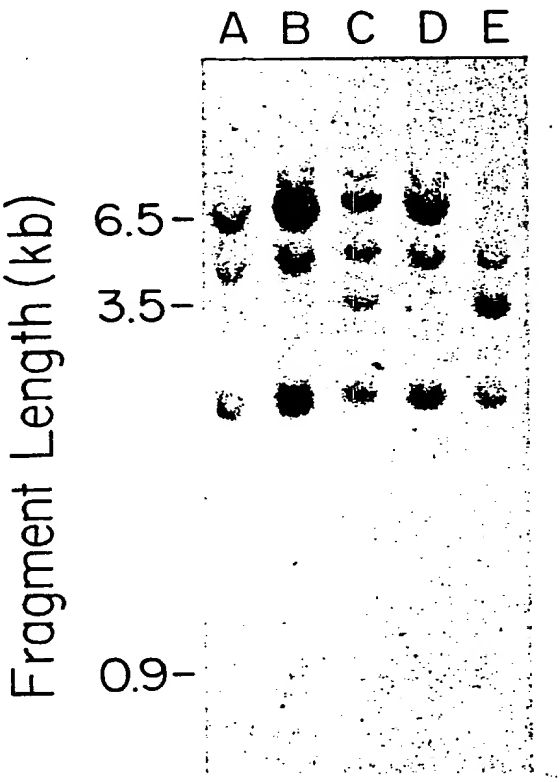

FIGURE 9

Southern Blot Analysis of Complete Androgen Insensitivity Syndrome Patients